

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: COLOTTA, Francesco MUZIO, Marta MANTOVANI, Alberto
 - (ii) TITLE OF INVENTION: INTERLEUKIN-1 ANTAGONIST, DNA ENCODING SAME,

AND ANTIBODIES THERETO

- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BROWDY AND NEIMARK
 - (B) STREET: 419 Seventh Street, N.W., Suite 300
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk

 - (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/476,860
 - (B) FILING DATE: 07-JUN-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: IT MI 94 A 002097
 - (B) FILING DATE: 13-OCT-1994
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: YUN, Allen C.
 - (B) REGISTRATION NUMBER: 37,971
 - (C) REFERENCE/DOCKET NUMBER: COLOTTA=1A
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-628-5197
 - (B) TELEFAX: 202-737-3528
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA
 - (iii) HYPOTHETICAL: NO
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: RT-PCR oligonucleotide named IRA5
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGACTTGTA TGAAGAAGGA GGTGG

25

(2) INFO	RMATION FOR SEQ ID NO: 2:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA	
(iii)	HYPOTHETICAL: NO	
(ix)	FEATURE: (D) OTHER INFORMATION: RT-PCR oligonucleotide corresponding to 60-79 of B-actin	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
GCGCTCGT	CG TCGACAACGG	20
(2) INFO	RMATION FOR SEQ ID NO: 3:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA	
(iii)	HYPOTHETICAL: NO	
(ix)	FEATURE: (D) OTHER INFORMATION: RT-PCR backward oligonucleotide complementary to 430-449	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
GATAGACA	AC GTACATGGCT G	21
(2) INFO	RMATION FOR SEQ ID NO: 4:	
	SEQUENCE CHARACTERISTICS: (A) LENGTH: 87 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	MOLECULE TYPE: DNA	
	HYPOTHETICAL: NO	
(1X)	FEATURE: (D) OTHER INFORMATION: Sequence of sIL-1ra not in common	
(ix)	FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 2486	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
GAATTCCG	GG CTGCAGTCAC AGA ATG GAA ATC TGC AGA GGC CTC CGC AGT Met Glu Ile Cys Arg Gly Leu Arg Ser 1 5	50

CAC CTA ATC ACT CTC CTC CTC TTC CTG TTC CAT TCA G His Leu Ile Thr Leu Leu Leu Phe Leu Phe His Ser 10 15 20	87
(2) INFORMATION FOR SEQ ID NO: 5:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 21 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: protein	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
Met Glu Ile Cys Arg Gly Leu Arg Ser His Leu Ile Thr Leu Leu Leu 1 5 10 15	
Phe Leu Phe His Ser 20	
(2) INFORMATION FOR SEQ ID NO: 6:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA	
(iii) HYPOTHETICAL: NO	
<pre>(ix) FEATURE: (D) OTHER INFORMATION: Sequence of intracellular IL-1ra</pre>	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 3341	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
CAGAAGACCT CCTGTCCTAT GAGGCCCTCC CC ATG GCT TTA G Met Ala Leu 1	42
(2) INFORMATION FOR SEQ ID NO: 7:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA	

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS (B) LOCATION: 1..468

	(1x) FEATURE: (D) OTHER	INFORMATION: Sequence of intracellular IL-1ra typeII not in common									
	(ix) FEATURE: (A) NAME/K (B) LOCATI	KEY: CDS ION: 33104									
	(xi) SEQUENCE DE	ESCRIPTION: SEQ ID NO: 7:									
CAG	AAGACCT CCTGTCCTA	AT GAGGCCCTCC CC ATG GCT TTA GCT GAC TTG TAT Met Ala Leu Ala Asp Leu Tyr 1 5	53								
		GGA GGA GGA GGT GAA GAC AAT GCT GAC TCA Gly Gly Glu Gly Glu Asp Asn Ala Asp Ser 15 20	101								
AAG Lys	G		105								
(2)	INFORMATION FOR	SEQ ID NO: 8:									
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 24 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear										
	(ii) MOLECULE TY	YPE: protein									
	(xi) SEQUENCE DE	ESCRIPTION: SEQ ID NO: 8:									
Met 1	Ala Leu Ala Asp 5	Leu Tyr Glu Glu Gly Gly Gly Gly Glu 10 15									
Gly	Glu Asp Asn Ala 20	Asp Ser Lys									
(2)	INFORMATION FOR	SEQ ID NO: 9:									
	(B) TYPE: (C) STRAND	HARACTERISTICS: H: 474 base pairs nucleic acid DEDNESS: single DGY: linear									
	(ii) MOLECULE TY	YPE: DNA									
	(iii) HYPOTHETICA	AL: NO									
	(ix) FEATURE: (D) OTHER	INFORMATION: Common IL-1ra sequence; a nucleotid was added in the first position, for computer preason, in order to encode the first amino acid and further in order to avoid the creation of a codon in the inner region of the sequence	ogram Glu								

(xi)	SE	QUEN	CE DI	ESCR:	IPTI	ON: S	SEQ :	ID NO	D: 9	:				
													CAA Gln 15	48
													AAC Asn	96
													GAA Glu	144
													GGA Gly	192
													GAG Glu	240
													AAC Asn 95	288
													CCC Pro	336
													ACA Thr	384
													GAA Glu	432
Met		Thr	Lys	Phe	Tyr	Phe	Gln		GAC Asp 155		TAG	rac		474

- (2) INFORMATION FOR SEQ ID NO: 10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 amino acids

 - (B) TYPE: amino acid(D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Glu Thr Ile Cys Arg Pro Ser Gly Arg Lys Ser Ser Lys Met Gln Ala

Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe Tyr Leu Arg Asn Asn

Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn Val Asn Leu Glu Glu

Lys Ile Asp Val Val Pro Ile Glu Pro His Ala Leu Phe Leu Gly Ile 50 55 60

His Gly Gly Lys Met Cys Leu Ser Cys Val Lys Ser Gly Asp Glu Thr 65 70 75 80

Arg Leu Gln Leu Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn Arg 85 90 95

Lys Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser Asp Ser Gly Pro Thr 100 105 110

Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp Phe Leu Cys Thr Ala 115 120 125

Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn Met Pro Asp Glu Gly 130 135 140

Val Met Val Thr Lys Phe Tyr Phe Gln Glu Asp Glu 145 150 155

- (2) INFORMATION FOR SEQ ID NO: 11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (v) FRAGMENT TYPE: internal
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: A portion of the intracellular IL-1ra typeII not in common
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Ala Asp Leu Tyr Glu Glu Gly Gly Gly Gly Gly Glu Gly Glu Asp
1 10 15

Asn Ala Asp Ser Lys 20

- (2) INFORMATION FOR SEQ ID NO: 12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA
 - (iii) HYPOTHETICAL: NO
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Intracellular IL-1ra typeII

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 34..573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CAGAAGGACC TCCTGTCCTA TGAGGCCCTC CCC ATG GCT TTA GCT GAC TTG TAT 54											
CAGAAGGACC TCCTGTCCTA TGAGGCCCTC CCC ATG GCT TTA GCT GAC TTG TAT Met Ala Leu Ala Asp Leu Tyr 1 5											
		GAA GGT GAA GAC . Glu Gly Glu Asp .									
		GGG AGA AAA TCC : Gly Arg Lys Ser : 35									
		CAG AAG ACC TTC Gln Lys Thr Phe 50									
		CAA GGA CCA AAT (Gln Gly Pro Asn) 65									
		GAG CCT CAT GCT Glu Pro His Ala :									
		TCC TGT GTC AAG Ser Cys Val Lys									
		AAC ATC ACT GAC Asn Ile Thr Asp 1115									
		TTC ATC CGC TCA (Phe Ile Arg Ser 1									
Thr Thr Ser Phe G		TGC CCC GGT TGG C Cys Pro Gly Trp									
		AGC CTC ACC AAT . Ser Leu Thr Asn 1									
		TTC CAG GAG GAC Phe Gln Glu Asp									

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

	(xi)	SEG	QUEN	CE DI	ESCR	PTIC	ON: 5	SEQ :	ID NO): 13	3:				
Met 1	Ala	Leu	Ala	Asp 5	Leu	Tyr	Glu	Glu	Gly 10	Gly	Gly	Gly	Gly	Gly 15	Glı
Gly	Glu	Asp	Asn 20	Ala	Asp	Ser	Lys	Glu 25	Thr	Ile	Cys	Arg	Pro 30	Ser	Gly
Arg	Lys	Ser 35	Ser	Lys	Met	Gln	Ala 40	Phe	Arg	Ile	Trp	Asp 45	Val	Asn	Glr
Lys	Thr 50	Phe	Tyr	Leu	Arg	Asn 55	Asn	Gln	Leu	Val	Ala 60	Gly	Tyr	Leu	Glr
Gly 65	Pro	Asn	Val	Asn	Leu 70	Glu	Glu	Lys	Ile	Asp 75	Val	Val	Pro	Ile	Gl: 80
Pro	His	Ala	Leu	Phe 85	Leu	Gly	Ile	His	Gly 90	Gly	Lys	Met	Cys	Leu 95	Sei
Cys	Val	Lys	Ser 100	Gly	Asp	Glu	Thr	Arg 105	Leu	Gln	Leu	Glu	Ala 110	Val	Ası
Ile	Thr	Asp 115	Leu	Ser	Glu	Asn	Arg 120	Lys	Gln	Asp	Lys	Arg 125	Phe	Ala	Phe
Ile	Arg 130	Ser	Asp	Ser	Gly	Pro 135	Thr	Thr	Ser	Phe	Glu 140	Ser	Ala	Ala	Cys
Pro 145	Gly	Trp	Phe	Leu	Cys 150	Thr	Ala	Met	Glu	Ala 155	Asp	Gln	Pro	Val	Se:
Leu	Thr	Asn	Met	Pro 165	Asp	Glu	Gly	Val	Met 170	Val	Thr	Lys	Phe	Tyr 175	Phe

(2) INFORMATION FOR SEQ ID NO:14:

180

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTGAGTCAG CATTGTCTTC A

Gln Glu Asp Glu

21

- (2) INFORMATION FOR SEQ ID NO:15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

	(xi)	SE	EQUENCE	E DES	CRI	PTION:	SE	EQ II	NO:	15:							
CTGA	CTTG	ΓA	TGAAGA	AAGG	GG:	rgg											25
(2)	INFO	RMZ	ATION H	FOR S	EQ I	ID NO:	16:	:	,								
	(i)	(EQUENCE (A) LEM (B) TYM (C) STM (D) TOM	NGTH: PE: & RANDE	21 mino DNES	amino acid SS: si	ac l ngl	cids									
	(ii)	MC	DLECULE	TYP	E: E	peptid	e										
	(xi)	SE	EQUENCE	E DES	CRI	PTION:	SE	EQ II	NO:	16:							
	Ala 1	As	p Leu	Tyr	Glu 5	Glu G	ly	Gly	Gly	Gly 10	Gly	Gly	Gl	u Gly	/ Gl		р
	Asn	Al	a Asp	Ser 20	Lys												
(2)	INFO	RM#	ATION E	FOR S	EQ]	D NO:	17:	:									
	(i)	(QUENCE (A) LEN (B) TYE (C) STE (D) TOE	NGTH: PE: r RANDE	317 ucle DNES	76 bas eic ac SS: si	e p id ngl	airs									
	(ii)	MC	LECULE	E TYF	E: 0	DNA											
	(xi)	SE	QUENCE	E DES	CRI	PTION:	SE	EQ II	NO:	17:							
CAGA	AGAC	CT	CCTGTC	CTAI	' GAG	GCCCT	CC	CCAT	'GGC'I	TT	AGGT	AGC	rc	CTTC	CACI	CT	60
CATI	TTTT	CA	CCTGAG	raaa s	' GAG	BAGAGG	AA	AATG	TCT	ACA	ATTG	TGT	FT .	ATCA	AATG	CT	120
TTCA	GGCT	СТ	GGTGAG	CAAC	CGI	CCAGG	AA	AATG	TCA	AGC	GCAT	GAG	CT	CCAG	3CCI	TGT	180
CTGG	GGGA	rc	TGGGC	ACGGG	GAC	GCATC	CA	TGGG	AGAC	CCA	TGCAG	GCA	CT	CTGAC	GCA	AGG	240
GGCT	GCAA	ЭC	TAGTGO	CCTGC	TGC	GGCAG	CA	GGTG	AAC	AGA	GAGGT	GTA	AC '	TGCT	GTGA	ACA	300
GAAG	TCATO	3G	AGTCCT	TGGA	GTO	TGAGG	GT	CATT	TTCC	CAC	TGTTG	ATA	ξA.	ATAGO	GAA	AAT	360



TGGTGAAATA GCCCTGTTAA ATGAGAGAAA GAACAGTGTG AGCTCAATGA GAAATACTAA

TAGAATGTGG CACTGAGCCA CAAGGTCTGA GGGTTGATTG ATAAGGAAGG GTGGGGACTG

TGGAGAATTA AGGGCTTGGC ACAGGTCAGT TCCACCAGTT GTCACAAGAG AATGCAGGCT

CAGGTGGCCA GAACTTCTCG CTTTTCCAGA AGAGTCCGAT ATTCTGATTT CATTATATAT

AGTATTCTGA TTAAACCAGA CAATAAAGCA AGCAGATAAA ATATTTAAAG TATAAGCTGC

CAGTTTGCAA CCTCCGGTTA GGATTTGTGT GGGGCAAAGA AAAAAACTCT CAGGATCATT

GGTATGTAGA CTCTAATTTT AAGTTTCTAA TTTAAAATTG GCCCCTGAGG CTGGGCGTGG

TGGCTCACAC CTGTAATCCC AGCATTTTGG GAGGCCAAGG TGGGTGGATC TCTTGAGGTC

420

480

540

600

660

720

780

840

AAGAGTTCAA	GGCCTGCCTG	GCCAACATGG	TGAAACCCTG	TCTCTATTAA	AAATACAAAA	900
ATTAGCTGGG	CATGGTGGTG	CATGTCTGCA	ATCTTAGCTA	CTTGGGTAGC	TAAGGCAGGA	960
GAATTGCTGG	AACCCGGGAG	GTAGAGGTTG	CAGTGAATGG	AGATCACACC	ACTGCACTCC	1020
AGTCTGGGCA	ATAGAGAGAG	ACGCTCTCTC	ТАААААААА	TATGTAAAGA	TAAATAAAAT	1080
GAAATAAAAT	AGGCCTCTAA	TGAGCAGGCC	ATTCTCCTTT	CTGGGTCTTA	CTTTCCTTGC	1140
ACTCCTTTCT	GGGTGTTAAG	AGGAGGTCTA	GAGGAAGCTG	GACAACTCTT	AGCTTGTAGT	1200
AAGCACAGTG	GAAGTATCAG	CTCTTAATGG	GTCATGGACA	CGTTACGAAG	CTAGGCGCCG	1260
TGCTGAGCAC	TTTACATGGT	TTATCCCACT	GAACCCTCTC	AATAACCCTA	TGAGGAAGGG	1320
CTATTATTGC	TCACATTTTC	AGAAGAGGAA	ATGGATATAG	AGAGATTAGA	TAATTTGCCC	1380
ATGGCCAGAC	AGCTAGTATA	AGAGGAGGAG	GTGGATTGAC	TGCAGACATT	CTGTCTTCAA	1440
ACCACTACAC	TATGCTATGG	AGGCACAGAG	ACTTAATGAA	ATCATGGAGA	GGGGAATTGC	1500
TTTGTCAACC	ACAAGCAGTT	ATTCCGGGGG	CAGCAGATCC	TCCCCTGTCC	CCCAGTGGTA	1560
CAATGGTCCC	TGGTGGGTTG	TGCTACAATG	TTAGCCCATG	GTCTTATGTG	TTTTTCAAAT	1620
GTGTAAAGTA	GGATGCTGGA	ACCACTCTTA	GAACCAGATA	CCAATACATT	GTGAAGAAAT	1680
AAATCTCTGT	GCTTAAAACT	GGTTCATCCC	AAAATATTTT	GAACTGACAC	ACAATAGGTG	1740
СТАААТАААТ	GTGTGTTAAC	TTGAATTGGA	TTGAATTCGG	GAAAAAGTG	CAATAAGCTT	1800
AGTGAAGACA	CCATGTTCCC	TGGGTAGAGG	AACCACATTC	TCCATATAAG	GCCAGGAGTA	1860
TGGGAGGTAT	CAATGTTTGC	CCAGCACAGA	ACAGGGTGCC	AAGAAGAGAA	AAGTTGACGG	1920
GGTGCATACT	CTGACTGGAA	ACTGGAAGGG	TGAGAACAGA	GGGTAAAGGA	TAGAGATGGA	1980
ACCATGTGCA	TACACTTTGT	GTTACCTTGG	ACAAGTCATT	CATTTCTCTG	GACCTCTGCT	2040
TTCTCTCTAC	ACAATGGGGT	CCCACCACTT	CCCTTACAGC	TGACTTGTAT	GAAGAAGGAG	2100
GTGGAGGAGG	AGGAGAAGGT	GAAGACAATG	CTGACTCAAA	GGGTAAATTA	TTTTTAGGAT	2160
CCAAGTTTGA	AAACAATTTT	AGGCTACTAG	ATATGAACAA	CATCTTGATT	ATGTAGTTGA	2220
AGGAAATTAA	AGATGAATGG	TTTAATTAAA	AATTAATCAG	AATGAAAACG	ATTGATTACT	2280
AATATATCTG	CAATGGTTTA	TTTTCCTGAG	TGGCAGACTC	ACTAAGGTTT	TTGAATACTC	2340
CTGTGTGATT	GCTCTATGTA	TGTATGTATG	TATGTATGTA	TGCATGTATC	TATCTATCTG	2400
TTGTCTAATA	GAATGGATCA	CATCTCTGCT	ААТАААААСА	CTACACTGGC	AGGGTACAAT	2460
TATAATCATT	AACTGTGCCT	GGAATTTGCA	GCAGCAGCCA	CCAGAGGTAC	CAGTGCCCTT	2520
TAAGGGTTCA	TAATTTAGAA	TAATCCAATT	ATCTGAGTTT	TTCAGGGACT	GAGGGGTTTG	2580
GCAAGGTGTA	GAACTTTCAG	TAATAAAGTC	AAGAAAGTCC	TGGACAAACC	AAGGTAGTTG	2640
GTCACTCTAG	TCCATAACCA	GGTAAAGAGC	TTTCCCTGTA	ACCTGTGTAA	GGTTTTAGAA	2700
TCATTTCTTT	CCTTATTACC	AAAAATCCTC	CCCAAATTTT	CAAGAAATTA	TGAACTAAAT	2760

AGTTACTCTA	TGAGATAGGA	GTTCAGCCCA	AAAGAAACAC	CATAAGAACA	AATATAATTC	2820
TTĠCTTATGT	TAACCATGCA	ATGAAGCAGA	GAGAAAAAGT	CAGTGGCCTC	TTTAGGAGGA	2880
CTGTAGTGTG	GGAAGAAATA	ACTAAACTGG	GTTTCAATCC	TGGCCTGGCC	AGGATCTGGA	2940
GCAAGTGAGT	TAATCTTTCA	AAGCCTTGAG	TAGTTTATAA	AAGAATGGCC	ACTCCATAGA	3000
CAGAGTAGCC	TGAACCTTGA	GTTCTTCTAT	AAAGTCACTA	TGAATTTATA	CTCATTTTGA	3060
AAGTGGGTGT	CAATATGTCT	GTCCACTTTG	CACAGCTGTT	ATGTGGACAA	AAGGAGATCT	3120
GTGTGAAAGT	GTAACACAGA	GCCTAAACTA	TAACAGGTAA	GCAACACAGT	TGTCCC	3176